**S4 Table.** Boolean modelling of Activator-Inhibitor combinations.

Parameters p

|  |  |
| --- | --- |
| Activators |  |
| *Aa* | <0.001 |
| *Modified Ca* | <0.001 |
| *Modified Xa* | <0.001 |
| *Modified Ta* | <0.001 |
| *Ea* | 0.001 |
|  |  |
| *K* | <0.001 |
|  |  |
| Inhibitors |  |
| *Modified Ai* | <0.001 |
| *Pi* | <0.001 |
| *Modified Xi* | 0.001 |
| *Modified Ti* | 0.030 |
| *Ei* | 0.201 |

Variance explained (adjusted R2): 70.5%

Log likelihood of data: -2282.93 (same data as used in in S2 Table and S3 Table)

The model shown considered the Activator-Inhibitor combination effects shown in Table S3 (*Ca ~ Ai, TXa ~ Ai, THa ~ THi, TXa ~ TXi).* The data for wells were modified according to this scheme, for example a well containing both *THi* and *THa* was recoded as containing neither (i.e. equivalent to a control well containing resting platelets), requiring the modification of the coding for 6 of the 10 parameters in the model.

The Boolean model is more constrained, since it assumes all-or-nothing effects. This contrasts with the linear model in S3 Table, where the fitting of a quantitative interaction term for the Activator-Inhibitor combinationsallows some interactions to be very strong and others to be relatively weak. While the Boolean model apparently has fewer degrees of freedom than that shown in Table S3, the coding of the model into the data means that it has somewhere between five fewer degrees of freedom, and equal degrees of freedom to the quantitative model. While the Boolean model is a much better fit than the model assuming no activator-inhibitor combinations (S2 Table, p<0.001), it is not as good a fit as the regression model allowing quantitative effects (S3 Table). Even assuming that the quantitative model (Table S3) has five more degrees of freedom, it still represents a much better fit to the data (-2lnL or (χ2)difference of Table S2 and S3 = 53.26, p<0.001 with five degrees of freedom ).